IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Baker et al.	Docket No:	39780-2830P1C47
Serial No:	10/015,671	Group Art Unit:	1647
Filed:	December 11, 2001	Examiner:	Rachel B. Kapust

For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
Washington, D.C. 20231

DECLARATION OF WILLIAM WOOD, Ph.D. UNDER 37 CFR 1.131

I, William Wood, Ph.D. do hereby declare and say as follows:

1. I am Director and Staff Scientist at the Department of Bioinformatics, of Genentech, Inc., South San Francisco, CA 94080.

2. I am one of the inventors of the above-identified application.

3. I have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by U.S. Patent Publication No. 2003/0096951 (Jacobs *et al.*, publication date May 22, 2003 and effective filing date August 14, 1998).

4. I, along with other inventors of this application, conceived and reduced to practice the polypeptide designated as PRO1244 (SEQ ID NO:130) claimed in the above-identified application in the United States prior to August 14, 1998.

5. At the time the PRO1244 polypeptide was cloned and sequenced I was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA that encoded PRO1244 polypeptide (SEQ ID NO:130) claimed in the above-identified application.

6. A cDNA clone, referred to as DNA64883-1526 in the above-identified application, was identified as encoding the PRO1244 polypeptide.

7. The full length of the cDNA clone is shown in Figure 73 of the above-identified application. The full-length cDNA sequence has 2213 nucleotide residues. The full

length of the PRO1244 peptide encoded by DNA64883-1526 is shown in Figure 74 of the above-identified application. The full-length PRO1244 polypeptide has 335 amino acid residues.

8. Copies of the pages from the GSeqEdit database which report the cloning and sequencing data for the PRO1244 polypeptide sequence and its encoding nucleic acid sequence are attached to this declaration (with the dates redacted) as Exhibit A.

9. The GSeqEdit report shows the full-length nucleic acid sequence for DNA-64883-1526 (identified as "DNA-64883") and the full-length PRO1244 polypeptide encoded by DNA 64883. Both the DNA-64883 and the PRO1244 polypeptide sequences were obtained prior to August 14, 1998.

10. The DNA-64883 sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 129 disclosed in the above-identified application.

11. The beginning of the cDNA sequence corresponding to SEQ ID NO: 129 in the above-identified application is shown on page 1 of the GSeqEdit database report and the location of the first nucleotide is marked with "^insert starts here" and an arrow. The location of the last nucleotide corresponding to SEQ ID NO: 129 is shown on page 11 and is marked with an arrow.

12. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 130 disclosed in the above-identified application.

13. The first 26 amino acid residues of the PRO1244 polypeptide (SEQ ID NO:130) encoded by the cDNA (DNA-64883) are also shown on page 1 of the GSeqEdit report and the remaining 309 residues appear on pages 2-6 of the report.

14. Exhibit A clearly shows that both the full-length DNA-64883 sequence and the full-length PRO1244 polypeptide sequence disclosed in the above-identified application were obtained prior to August 14, 1998.

15. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and

the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

William Wood

6/1/04
Date

SV 2037583 v1
6/9/04 1:21 PM (39780.2830)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Baker et al.	Docket No:	39780-2830P1C47
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For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
Washington, D.C. 20231

DECLARATION OF AUDREY GODDARD, Ph.D. UNDER 37 CFR 1.131

I, Audrey Goddard, Ph.D. do hereby declare and say as follows:

1. I am Senior Clinical Scientist at the Diagnostics, Development Sciences Department of Genentech, Inc., South San Francisco, CA 94080.

2. I am one of the inventors of the above-identified application.

3. I have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by U.S. Patent Publication No. 2003/0096951 (Jacobs *et al.*, publication date May 22, 2003 and effective filing date August 14, 1998).

4. I, along with other inventors of this application, conceived and reduced to practice the polypeptide designated as PRO1244 (SEQ ID NO:130) claimed in the above-identified application in the United States prior to August 14, 1998.

5. At the time the PRO1244 polypeptide was cloned and sequenced I was responsible for overseeing the sequencing of novel polypeptides, including the PRO1244 polypeptide (SEQ ID NO:130) claimed in the above-identified application.

6. A cDNA clone, referred to as DNA64883-1526 in the above-identified application, was identified as encoding the PRO1244 polypeptide.

7. The full length of the cDNA clone is shown in Figure 73 of the above-identified application. The full-length cDNA sequence has 2213 nucleotide residues. The full length of the PRO1244 peptide encoded by DNA64883-1526 is shown in Figure 74 of

the above-identified application. The full-length PRO1244 polypeptide has 335 amino acid residues.

8. Copies of the pages from the GSeqEdit database which report the cloning and sequencing data for the PRO1244 polypeptide sequence and its encoding nucleic acid sequence are attached to this declaration (with the dates redacted) as Exhibit A.

9. The GSeqEdit report shows the full-length nucleic acid sequence for DNA-64883-1526 (identified as "DNA-64883") and the full-length PRO1244 polypeptide encoded by DNA 64883. Both the DNA-64883 and the PRO1244 polypeptide sequences were obtained prior to August 14, 1998.

10. The DNA-64883 sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 129 disclosed in the above-identified application.

11. The beginning of the cDNA sequence corresponding to SEQ ID NO: 129 in the above-identified application is shown on page 1 of the GSeqEdit database report and the location of the first nucleotide is marked with "^insert starts here" and an arrow. The location of the last nucleotide corresponding to SEQ ID NO: 129 is shown on page 11 and is marked with an arrow.

12. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 130 disclosed in the above-identified application.

13. The first 26 amino acid residues of the PRO1244 polypeptide (SEQ ID NO:130) encoded by the cDNA (DNA-64883) are also shown on page 1 of the GSeqEdit report and the remaining 309 residues appear on pages 2-6 of the report.

14. Exhibit A clearly shows that both the full-length DNA-64883 sequence and the full-length PRO1244 polypeptide sequence disclosed in the above-identified application were obtained prior to August 14, 1998.

15. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001

of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

A. Goddard

Audrey Goddard

6/17/04

Date

SV 2037583 v1
6/15/04 3:03 PM (39780.2830)

Exhibit A
to Declarations of Audrey Goddard and William Wood under 37 CFR 1.131

GSeqEdit Database Report

>[redacted]
>DNA64883 [Full]
>510 Sites [All Sites]
>[redacted] DNA64883 wiw GSeqEdit
>[redacted] DNA64883 zemin GSeqEdit
>[redacted] DNA64883 goddarda GSeqEdit
>[redacted] DNA64883 sheldens GSeqEdit
>HBN64883.seq, sequenced at ABI/ACGT by Peter Ma and Ellson Chen
>human ortholog of implantation-associated protein - Rattus

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                                                             nlaIII
             mnlI                                            mslI
            taqI                                            styI
           xhoI                   thaI                      ncoI
           tliI                   fnuDII/mvnI               dsaI         tseI
           smlI                  hinPI   aciI               btgI/bstDSI  fnu4HI/bsoFI
           paeR7I  mwoI        tseI bstUI[M.hhaI-]          bstXI        bbvI                   dde
      tsp509I[M.ecoRI-]        fnu4HI/bsoFI                 bsaJI       hinPI            taiI   bsp
     ecoRI     avaI[M.taqI-]   bbvI bsh1236I             tsp45I         hhaI/cfoI        maeII/hpyC
     apoI   mwoI bseRI      nlaIII  hhaI/cfoI        bsmAI maeIII       haeII         hpy99I   mnlI
1 CGGAATTCGG CTCGAGGAGC GAACATGGCA GCGCGTTGGC GGTTTTGGTG TGTCTCTGTG ACCATGGTGG TGGCGCTGCT CATCGTTTGC GACGTTCCCT
  GCCTTAAGCC GAGCTCCTCG CTTGTACCGT CGCGCAACCG CCAAAACCAC ACAGAGACAC TGGTACCACC ACCGCGACGA GTAGCAAACG CTGCAAGGGA
1                 ↑          M  A   A  R  W  R   F  W  C   V  S  V   T  M  V  V   A  L  L   I  V  C   D  V  P  S
                  ^insert starts here
                             ^MET
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      mnlI                                                  aluI
   alwNI[dcm-]                                              pvuII
    alw26I/bsmAI          bsaXI        hpy188I             mspA1I/nspBII                                        bsmAI
101 CAGCCTCTGC CCAAAGAAAG AAGGAGATGG TGTTATCTGA AAAGGTTAGT CAGCTGATGG AATGGACTAA CAAAAGACCT GTAATAAGAA TGAATGGAGA
    GTCGGAGACG GGTTTCTTTC TTCCTCTACC ACAATAGACT TTTCCAATCA GTCGACTACC TTACCTGATT GTTTTCTGGA CATTATTCTT ACTTACCTCT
 27   A  S  A   Q  R  K   K  E  M  V   L  S  E   K  V  S   Q  L  M  E   W  T  N   K  R  P   V  I  R  M   N  G  D

                                                        tspRI               bst4CI/hpyCH4III    cac8I
                                                        btsI                ahdI/eam1105I     cac8I
        hpy99I                      tsp509I             nlaIII              hpyCH4V tspRI          hpyCH4V al
201 CAAGTTCCGT CGCCTTGTGA AAGCCCCACC GAGAAATTAC TCCGTTATCG TCATGTTCAC TGCTCTCCAA CTGCATAGAC AGTGTGTCGT TTGCAAGCAA
    GTTCAAGGCA GCGGAACACT TTCGGGGTGG CTCTTTAATG AGGCAATAGC AGTACAAGTG ACGAGAGGTT GACGTATCTG TCACACAGCA AACGTTCGTT
 60  K  F  R   R  L  V  K   A  P  P   R  N  Y   S  V  I  V   M  F  T   A  L  Q   L  H  R  Q   C  V  V   C  K  Q
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                    scrFI[dcm-]
                    pspGI
                    mvaI
                    ecoRII[dcm-]
                    dsaV[dcm-]
                    bstNI
                    bssKI[dcm-]
                    apyI[dcm+]
                  sau3AI
                  mboI/ndeII[dam-]
                  dpnII[dam-]
                  dpnI[dam+]
                  alwI[dam-]       scrFI[dcm-]
                 bstYI/xhoII       pspGI
                alwNI[dcm-]        mvaI                                  nlaIII
                alw26I/bsmAI       ecoRII[dcm-]                          styI
           tsp509I[M.ecoRI-]       dsaV[dcm-]       hpyCH4V              ncoI
       ecoRI pflMI[dcm-]           bstNI baeI    tspRI                   dsaI
       apoI  bslI[dcm-]            bssKI[dcm-]  bsrI bsmI hphI          btgI/bstDSI
    mboII   hpy188III              apyI[dcm+] bpmI/gsuI[dcm-]           bsaJI                    hpy18
301 GCTGATGAAG AATTCCAGAT CCTGGCAAAC TCCTGGCGAT ACTCCAGTGC ATTCACCAAC AGGATATTTT TTGCCATGGT GGATTTTGAT GAAGGCTCTG
    CGACTACTTC TTAAGGTCTA GGACCGTTTG AGGACCGCTA TGAGGTCACG TAAGTGGTTG TCCTATAAAA AACGGTACCA CCTAAAACTA CTTCCGAGAC
 93 A  D  E  E  F  Q  I  L  A  N  S  W  R  Y  S  S  A  F  T  N  R  I  F  F  A  M  V  D  F  D  E  G  S  D
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                      tsp509I[M.ecoRI-]
                     ecoRI                                hpyCH4V
                sfaNI     apoI                            ecoNI
              hpy188I  nlaIII  aluI                       bslI        bslI       hphI     ndeI    maeIII     aciI
401 ATGTATTTCA GATGCTAAAC ATGAATTCAG CTCCAACTTT CATCAACTTT CCTGCAAAAG GGAAACCCAA ACGGGGTGAT ACATATGAGT TACAGGTGCG
    TACATAAAGT CTACGATTTG TACTTAAGTC GAGGTTGAAA GTAGTTGAAA GGACGTTTTC CCTTTGGGTT TGCCCCACTA TGTATACTCA ATGTCCACGC
127  V  F  Q   M  L  N   M  N  S  A   P  T  F   I  N  F   P  A  K  G   K  P  K   R  G  D   T  Y  E  L   Q  V  R

                 ddeI[M.aluI-]
                 bspCNI      mspI   sau3AI
                 celII/espI  hpaII  mboI/ndeII[dam-]
                 blpI/bpu1102I scrFI[M.hpaII-]                                                     bsmFI
               aluI          nciI   dpnII[dam-]                                                    sau96I
              pvuII          dsaV   dpnI[dam+]                                                     nlaIV
              mspA1I/nspBII  bssKI alwI[dam-]                sspI                        tsp509I   avaII bslI
501 GGGTTTTTCA GCTGAGCAGA TTGCCCGGTG GATCGCCGAC AGAACTGATG TCAATATTAG AGTGATTAGA CCCCCAAATT ATGCTGGTCC CCTTATGTTG
    CCCAAAAAGT CGACTCGTCT AACGGGCCAC CTAGCGGCTG TCTTGACTAC AGTTATAATC TCACTAATCT GGGGGTTTAA TACGACCAGG GGAATACAAC
160 G  F  S   A  E  Q  I   A  R  W   I  A  D   R  T  D  V   N  I  R   V  I  R   P  P  N  Y   A  G  P   L  M  L

                                 taqI                                                                aluI
                                 sfuI                                                               tseI
                                 bstBI                                            fokI              fnu4HI/bsoFI
                                 bsiCI                     tsp509I   tru9I        bstF5I            bbvI
                          baeI   mboII mboII               apoI      mseI      bsrI       mwoI hpyCH4V
601 GGATTGCTTT TGGCTGTTAT TGGTGGACTT GTGTATCTTC GAAGAAGTAA TATGGAATTT CTCTTTAATA AAACTGGATG GGCTTTTGCA GCTTTGTGTT
    CCTAACGAAA ACCGACAATA ACCACCTGAA CACATAGAAG CTTCTTCATT ATACCTTAAA GAGAAATTAT TTTGACCTAC CCGAAAACGT CGAAACACAA
193 G  L  L  L   A  V  I   G  G  L   V  Y  L  R   R  S  N   M  E  F   L  F  N  K   T  G  W   A  F  A   A  L  C  F
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                                                                          nlaIII           nlaIII
                                                                          pciI             styI
                                                                          nspHI            ncoI
                                      sau96I                 bslI         nspI             dsaI
                                      avaII             tfiI              aflIII           btgI/bs
    cac8I      ahdI/eam1105I  nlaIV   mnlI      ndeI    hinfI        bsmFI      tsp509I   bsaJI
701 TTGTGCTTGC TATGACATCT GGTCAAATGT GGAACCATAT AAGAGGACCA CCATATGCCC ATAAGAATCC CCACACGGGA CATGTGAATT ATATCCATGG
    AACACGAACG ATACTGTAGA CCAGTTTACA CCTTGGTATA TTCTCCTGGT GGTATACGGG TATTCTTAGG GGTGTGCCCT GTACACTTAA TATAGGTACC
227  V  L  A   M  T  S   G  Q  M  W   N  H  I   R  G  P   P  Y  A  H   K  N  P   H  T  G   H  V  N  Y   I  H  G

                                                        ddeI                        tseI
                                                        eco81I                      fnu4HI/bsoFI
                                         tru9I          bsu36I/mstII/sauI           bbvI       hpy1
               bsrI      aluI       mboII  mseI     maeIII                          aluI      mnlI
801 AAGCAGTCAA GCCCAGTTTG TAGCTGAAAC ACACATTGTT CTTCTGTTTA ATGGTGGAGT TACCTTAGGA ATGGTGCTTT TATGTGAAGC TGCTACCTCT
    TTCGTCAGTT CGGGTCAAAC ATCGACTTTG TGTGTAACAA GAAGACAAAT TACCACCTCA ATGGAATCCT TACCACGAAA ATACACTTCG ACGATGGAGA
260  S  S  Q   A  Q  F  V   A  E  T   H  I  V   L  L  F  N   G  G  V   T  L  G   M  V  L  L   C  E  A   A  T  S

                                                                                    sau3AI
                                                                                    mboI/ndeII[dam
                                                                                    dpnII[dam-]
                                                                 sfaNI              dpnI[dam+]
                                                        eco57I   fokI              bstYI/xhoII
    nlaIII                                              mboII    bstF5I            bglII          nl
901 GACATGGATA TTGGAAAGCG AAAGATAATG TGTGTGGCTG GTATTGGACT TGTTGTATTA TTCTTCAGTT GGATGCTCTC TATTTTTAGA TCTAAATATC
    CTGTACCTAT AACCTTTCGC TTTCTATTAC ACACACCGAC CATAACCTGA ACAACATAAT AAGAAGTCAA CCTACGAGAG ATAAAAATCT AGATTTATAG
293 D  M  D  I   G  K  R   K  I  M   C  V  A  G   I  G  L   V  V  L   F  F  S  W   M  L  S   I  F  R   S  K  Y  H
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                                   bsmFI
                                   sau96I                          bsrI
                                   nlaIV                          rsaI
                                   avaII                      bpmI/gsuI[dcm-]
                              tru9I  ppuMI                    bsrI    csp6I
             aluI hpy188I     mseI   eco0109I/draII          tspRI   scaI      tsp509I
1001 ATGGCTACCC ATACAGCTTT CTGATGAGTT AAAAAGGTCC CAGAGATATA TAGACACTGG AGTACTGGAA ATTGAAAAAC GAAAATCGTG TGTGTTTGAA
     TACCGATGGG TATGTCGAAA GACTACTCAA TTTTTCCAGG GTCTCTATAT ATCTGTGACC TCATGACCTT TAACTTTTTG CTTTTAGCAC ACACAAACTT
327   G  Y  P   Y  S  F   L  M  S  O

                                                     tru9I
                                                     mseI    tru9I
      bsmI                                         ahaIII/draI      tru9I                         tru9I
     mboII hpyCH4V                  mnlI           swaI       mseI     mseI     mboII             mseI
1101 AAGAAGAATG CAACTTGTAT ATTTTGTATT ACCTCTTTTT TTCAAGTGAT TTAAATAGTT AATCATTTAA CCAAAGAAGA TGTGTAGTGC CTTAACAAGC
     TTCTTCTTAC GTTGAACATA TAAAACATAA TGGAGAAAAA AAGTTCACTA AATTTATCAA TTAGTAAATT GGTTTCTTCT ACACATCACG GAATTGTTCG

                mnlI
               ddeI                                       bsrI                    tsp509I     tru9I
               bspCNI                  mnlI tru9I      mboII tspRI             tru9I     rsaI tsp509I
      mnlI     hpy188I             tsp509I    mseI     earI/ksp632I            mseI      csp6I  mseI
1201 AATCCTCTGT CAAAATCTGA GGTATTTGAA AATAATTATC CTCTTAACCT TCTCTTCCCA GTGAACTTTA TGGAACATTT AATTTAGTAC AATTAAGTAT
     TTAGGAGACA GTTTTAGACT CCATAAACTT TTATTAATAG GAGAATTGGA AGAGAAGGGT CACTTGAAAT ACCTTGTAAA TTAAATCATG TTAATTCATA

                                                                tru9I
                                                                mseI
                                                               hpaI
     psiI   tsp509I                          aluI              hincII/hindII hpy188I          bslI
1301 ATTATAAAAA TTGTAAAACT ACTACTTTGT TTTAGTTAGA ACAAAGCTCA AAACTACTTT AGTTAACTTG GTCATCTGAT TTTATATTGC CTTATCCAAA
     TAATATTTTT AACATTTTGA TGATGAAACA AAATCAATCT TGTTTCGAGT TTTGATGAAA TCAATTGAAC CAGTAGACTA AAATATAACG GAATAGGTTT
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                          scrFI[dcm-]
                          pspGI
                          mvaI
                          ecoRII[dcm-]
                          dsaV[dcm-]
                          bstNI                                    tsp509I[M.ecoRI-]
                          bssKI[dcm-]                              xmnI
                          apyI[dcm+]                               ecoRI          mboII
                         sexAI                                     asp700     aluI     mslI        fokI
                    hpy188III          ndeI     maeIII            apoI      ddeI[M.aluI-]          bstF5I
1401 GATGGGGAAA GTAAGTCCTG ACCAGGTGTT CCCACATATG CCTGTTACAG ATAACTACAT TAGGAATTCA TTCTTAGCTT CTTCATCTTT GTGTGGATGT
     CTACCCCTTT CATTCAGGAC TGGTCCACAA GGGTGTATAC GGACAATGTC TATTGATGTA ATCCTTAAGT AAGAATCGAA GAAGTAGAAA CACACCTACA

                                                                                        taiI
                                                                                  hgiAI/aspHI
                                                                                  bsp1286
                                                          hpy188I                 bsiHKAI    rmaI  ddeI
     bstZ17I                                             mboII                  hpy188I   maeII/hpyCH4IV
     bst1107I                                           bpuAI                  eco57I    aflIII maeI  bspC
     accI       sfaNI                    tsp509I     nlaIII bbsI              mboII  bmyI btrI  bfaI mnlI
1501 GTATACTTTA CGCATCTTTC CTTTTGAGTA GAGAAATTAT GTGTGTCATG TGGTCTTCTG AAAATGGAAC ACCATTCTTC AGAGCACACG TCTAGCCCTC
     CATATGAAAT GCGTAGAAAG GAAAACTCAT CTCTTTAATA CACACAGTAC ACCAGAAGAC TTTTACCTTG TGGTAAGAAG TCTCGTGTGC AGATCGGGAG
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                                                                  tth111I/aspI
                                                                  pleI
            bseRI                                                 pflFI
           mnlI                           bpmI/gsuI[dcm-]         mlyI
          bseRI                         hinPI      ddeI           hinfI
     bst4CI/hpyCH4III mnlI  hpyCH4V     hhaI/cfoI  bspCNI        bsmAI     bsmAI
1601 AGCAAGACAG TTGTTTCTCC TCCTCCTTGC ATATTTCCTA CTGCGCTCCA GCCTGAGTGA TAGAGTGAGA CTCTGTCTCA AAAAAAAGTA TCTCTAAATA
     TCGTTCTGTC AACAAAGAGG AGGAGGAACG TATAAAGGAT GACGCGAGGT CGGACTCACT ATCTCACTCT GAGACAGAGT TTTTTTTCAT AGAGATTTAT

                               tru9I                                                                   tsp45I
                               mseI                            tfiI                                    hphI
          tsp509I             hpaI                 xmnI        hinfI                              tru9I maeIII
        psiI          smlI    hincII/hindII        asp700   hpy188I             ddeI              mseI bstEII
1701 CAGGATTATA ATTTCTGCTT GAGTATGGTG TTAACTACCT TGTATTTAGA AAGATTTCAG ATTCATTCCA TCTCCTTAGT TTTCTTTTAA GGTGACCCAT
     GTCCTAATAT TAAAGACGAA CTCATACCAC AATTGATGGA ACATAAATCT TTCTAAAGTC TAAGTAAGGT AGAGGAATCA AAAGAAAATT CCACTGGGTA

                                                                                                           dde
                  ddeI[M.aluI-]       maeIII        haeIII/palI                       tsp45I          rsaI
                 aluI               tspRI        nlaIII                   tsp509I     maeIII          csp6I
1801 CTGTGATAAA AATATAGCTT AGTGCTAAAA TCAGTGTAAC TTATACATGG CCTAAAATGT TTCTACAAAT TAGAGTTTGT CACTTATTCC ATTTGTACCT
     GACACTATTT TTATATCGAA TCACGATTTT AGTCACATTG AATATGTACC GGATTTTACA AAGATGTTTA ATCTCAAACA GTGAATAAGG TAAACATGGA
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                                        scrFI[dcm-]
                                        pspGI
                                        mvaI
                                        ecoRII[dcm-]
                                        dsaV[dcm-]
                                        bstNI
                                       haeIII/palI
                                      mscI/balI[dcm-]
                                      eaeI[dcm-]
                                      cfrI
                                    scrFI[dcm-]
                                    pspGI
                                    mvaI bssKI[dcm-]
                                    ecoRII[dcm-]   tsp45I
                                    dsaV[dcm-]     maeIII                                          bssS
                                    bstNI     hinPI                                                hpy18
                                    bssKI[dcm-]  tspRI                                            sau3AI
                                 pleI bslI[dcm-] hhaI/cfoI                          styI cac8I    mboI/nd
                  ddeI           mlyI bsaJI apyI[dcm+]                ddeI          haeIII/palI    dpnII[d
                  bspCNI         hinfI apyI[dcm+]  btsI               bspCNI     mnlI bsaJI        dpnI[da
1901 AAGAGAAAAA TAGGCTCAGT TAGAAAAGGA CTCCCTGGCC AGGCGCAGTG ACTTACGCCT GTAATCTCAG CACTTTGGGA GGCCAAGGCA GGCAGATCAC
     TTCTCTTTTT ATCCGAGTCA ATCTTTTCCT GAGGGACCGG TCCGCGTCAC TGAATGCGGA CATTAGAGTC GTGAAACCCT CCGGTTCCGT CCGTCTAGTG
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                                  mscI/ball[dcm-]
                                  eaeI[dcm-]
                                 scrFI[dcm-]
                                 pspGI
                                 mvaI
                                 ecoRII[dcm-]
                                 dsaV[dcm-]
                                 bstNI
                       bsmAI     bssKI[dcm-]
                     taqI   fokI  cfrI    nlaIII         bsmAI
           hpy188III  bsaI bstF5I haeIII/palI          esp3I                    aluI
mnlI         hpy188III  apyI[dcm+]   hphI       bsmBI                 tsp509I                nlaIV
2001 GAGGTCAGGA GTTCGAGACC ATCCTGGCCA ACATGGTGAA ACCCCGTCTC TACTAAAAAT ATAAAAATTA GCTGGGTGTG GTGGCAGGAG CCTGTAATCC
     CTCCAGTCCT CAAGCTCTGG TAGGACCGGT TGTACCACTT TGGGGCAGAG ATGATTTTTA TATTTTTAAT CGACCCACAC CACCGTCCTC GGACATTAGG

                                                                                                    scrFI[dcm-]
                                                                                                    pspGI
                                                                                                    mvaI
                                                                                                    ecoRII[dcm-]
                                                                                 tspRI              dsaV[dcm-]
                                                                          sau3AI   btsI             bstNI
                      ddeI        tfiI          hpy188III                mboI/ndeII[dam-]         bssKI[dcm-]
                      bspCNI      hinfI         ddeI                     dpnII[dam-] hpyCH4V      apyI[dcm+]
 aluI       mnlI  mnlI bssSI             bspCNI      mnlI    tspRI       dpnI[dam+] bsgI  bpmI/gsuI[dcm-]
2101 CAGCTACACA GGAGGCTGAG GCACGAGAAT CACTTGAACT CAGGAGATGG AGGTTTCAGT GAGCCGAGAT CACGCCACTG CACTCCAGCC TGGCAACAGA
     GTCGATGTGT CCTCCGACTC CGTGCTCTTA GTGAACTTGA GTCCTCTACC TCCAAAGTCA CTCGGCTCTA GTGCGGTGAC GTGAGGTCGG ACCGTTGTCT
```

```
                                                        fnu4HI/bsoFI
                                                       haeIII/palI
                                                      mcrI
                                                      eagI/xmaIII/eclXI
                                                      eaeI
                                                      cfrI
          pleI                                        bsiEI      rmaI
          mlyI                                      notI         maeI
          hinfI                                     fnu4HI/bsoFI bfaI
        bsmAI                                       aciI aciI  speI
2201 GCGAGACTCC ATCTCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAGGG CGGCCGCCGA CTAGTGAGC
     CGCTCTGAGG TAGAGTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTCCC GCCGGCGGCT GATCACTCG
```

> length: 2269

```
accI(GTMKAC):                    1501
aciI(CCGC):                      39 498 2250 2254
aflIII(ACRYGT):                  780 1586
ahaIII(TTTAAA):                  1150
ahdI(GACNNNNNGTC):               278 714
aluI(AGCT):                      152 300 429 510 690 822 888 1015 1345 1476 1816 2070 2102
alw26I(CAGNNNCTG):               101 316
alwI(GGATCNNNN):                 318 530
alwNI(CAGNNNCTG):                101 316
apoI(RAATTY):                    3 310 423 655 1464
apyI(CCWGG):                     321 332 1422 1934 1939 2023 2189
asp700(GAANNNNTTC):              1464 1749
aspHI(GWGCWC):                   1582
```